

### **INPUT SET: S23457.raw**

**This Raw Listing contains the General Information Section and up to the first 15 pages.**

## SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: COLOTTA, Francesco  
MUZIO, Marta  
MANTOVANI, Alberto

9 (ii) TITLE OF INVENTION: INTERLEUKIN-1 ANTAGONIST, DNA ENCODING SAME,  
10 AND ANTIBODIES THERETO

12 (iii) NUMBER OF SEQUENCES: 17

14 (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: BROWDY AND NEIMARK  
(B) STREET: 419 Seventh Street, N.W., Suite 300  
(C) CITY: Washington  
(D) STATE: D.C.  
(E) COUNTRY: USA  
(F) ZIP: 20004

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0. Version #1.30

28 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/476,860  
(B) FILING DATE: 07-JUN-1995

37 (vii) PTOB APPLICATION DATA:

(A) APPLICATION NUMBER: IT MI 94 A 002097  
(B) FILING DATE: 13-OCT-1994

40  
41 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: YUN, Allen C.  
(B) REGISTRATION NUMBER: 23

44 (C) REFERENCE/DOCKET NUMBER:  
45  
46 (ix) TELECOMMUNICATION INFORMATION:

**INPUT SET: S23457.raw**

47 (A) TELEPHONE: 202-628-5197  
48 (B) TELEFAX: 202-737-3528  
49  
50  
51 (2) INFORMATION FOR SEQ ID NO: 1:  
52  
53 (i) SEQUENCE CHARACTERISTICS:  
54 (A) LENGTH: 25 base pairs  
55 (B) TYPE: nucleic acid  
56 (C) STRANDEDNESS: single  
57 (D) TOPOLOGY: linear  
58  
59 (ii) MOLECULE TYPE: DNA  
60  
61 (iii) HYPOTHETICAL: NO  
62  
63 (ix) FEATURE:  
64 (D) OTHER INFORMATION: RT-PCR oligonucleotide named IRA5  
65  
66 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
67  
68 CTGACTTGTA TGAAGAAGGA GGTGG 25  
69  
70 (2) INFORMATION FOR SEQ ID NO: 2:  
71  
72 (i) SEQUENCE CHARACTERISTICS:  
73 (A) LENGTH: 20 base pairs  
74 (B) TYPE: nucleic acid  
75 (C) STRANDEDNESS: single  
76 (D) TOPOLOGY: linear  
77  
78 (ii) MOLECULE TYPE: DNA  
79  
80 (iii) HYPOTHETICAL: NO  
81  
82 (ix) FEATURE:  
83 (D) OTHER INFORMATION: RT-PCR oligonucleotide corresponding  
84 to 60-79 of B-actin  
85  
86 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
87  
88 GCGCTCGTCG TCGACAAACGG 20  
89  
90 (2) INFORMATION FOR SEQ ID NO: 3:  
91  
92 (i) SEQUENCE CHARACTERISTICS:  
93 (A) LENGTH: 21 base pairs  
94 (B) TYPE: nucleic acid  
95 (C) STRANDEDNESS: single  
96 (D) TOPOLOGY: linear  
97  
98 (ii) MOLECULE TYPE: DNA  
99

INPUT SET: S23457.raw

100 (iii) HYPOTHETICAL: NO  
101  
102 (ix) FEATURE:  
103 (D) OTHER INFORMATION: RT-PCR backward oligonucleotide  
104 complementary to 430-449  
105  
106 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
107  
108 GATAGACAAC GTACATGGCT G 21  
109  
110 (2) INFORMATION FOR SEQ ID NO: 4:  
111  
112 (i) SEQUENCE CHARACTERISTICS:  
113 (A) LENGTH: 87 base pairs  
114 (B) TYPE: nucleic acid  
115 (C) STRANDEDNESS: single  
116 (D) TOPOLOGY: linear  
117  
118 (ii) MOLECULE TYPE: DNA  
119  
120 (iii) HYPOTHETICAL: NO  
121  
122 (ix) FEATURE:  
123 (D) OTHER INFORMATION: Sequence of SIL-1ra not in common  
124  
125 (ix) FEATURE:  
126 (A) NAME/KEY: CDS  
127 (B) LOCATION: 24..86  
128  
129 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
130  
131 GAATTCCGGG CTGCAGTCAC AGA ATG GAA ATC TGC AGA GGC CTC CGC AGT 50  
132 Met Glu Ile Cys Arg Gly Leu Arg Ser  
133 1 5  
134  
135 CAC CTA ATC ACT CTC CTC CTC TTC CTG TTC CAT TCA G 87  
136 His Leu Ile Thr Leu Leu Phe Leu Phe His Ser  
137 10 15 20  
138  
139  
140 (2) INFORMATION FOR SEQ ID NO: 5:  
141  
142 (i) SEQUENCE CHARACTERISTICS:  
143 (A) LENGTH: 21 amino acids  
144 (B) TYPE: amino acid  
145 (D) TOPOLOGY: linear  
146  
147 (ii) MOLECULE TYPE: protein  
148  
149 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
150  
151 Met Glu Ile Cys Arg Gly Leu Arg Ser His Leu Ile Thr Leu Leu Leu 15  
152 1 5 10 15

INPUT SET: S23457.raw

153  
154 Phe Leu Phe His Ser  
155 20  
156  
157 (2) INFORMATION FOR SEQ ID NO: 6:  
158  
159 (i) SEQUENCE CHARACTERISTICS:  
160 (A) LENGTH: 42 base pairs  
161 (B) TYPE: nucleic acid  
162 (C) STRANDEDNESS: single  
163 (D) TOPOLOGY: linear  
164  
165 (ii) MOLECULE TYPE: DNA  
166  
167 (iii) HYPOTHETICAL: NO  
168  
169 (ix) FEATURE:  
170 (D) OTHER INFORMATION: Sequence of intracellular IL-1ra  
171 typeI not in common  
172  
173 (ix) FEATURE:  
174 (A) NAME/KEY: CDS  
175 (B) LOCATION: 33..41  
176  
177 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
178  
179 CAGAAAGACCT CCTGTCTTAT GAGGCCCTCC CC ATG GCT TTA G 42  
180 Met Ala Leu  
181 1  
182  
183  
184 (2) INFORMATION FOR SEQ ID NO: 7:  
185  
186 (i) SEQUENCE CHARACTERISTICS:  
187 (A) LENGTH: 105 base pairs  
188 (B) TYPE: nucleic acid  
189 (C) STRANDEDNESS: single  
190 (D) TOPOLOGY: linear  
191  
192 (ii) MOLECULE TYPE: DNA  
193  
194 (iii) HYPOTHETICAL: NO  
195  
196 (ix) FEATURE:  
197 (D) OTHER INFORMATION: Sequence of intracellular IL-1ra  
198 typeII not in common  
199  
200 (ix) FEATURE:  
201 (A) NAME/KEY: CDS  
202 (B) LOCATION: 33..104  
203  
204 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
205

INPUT SET: S23457.raw

206  
207 CAGAAAGACCT CCTGTCCTAT GAGGCCCTCC CC ATG GCT TTA GCT GAC TTG TAT 53  
208 Met Ala Leu Ala Asp Leu Tyr  
209 1 5  
210  
211 GAA GAA GGA GGT GGA GGA GGA GAA GGT GAA GAC AAT GCT GAC TCA 101  
212 Glu Glu Gly Gly Gly Gly Glu Asp Asn Ala Asp Ser  
213 10 15 20  
214  
215 AAG G 105  
216 Lys  
217  
218  
219 (2) INFORMATION FOR SEQ ID NO: 8:  
220  
221 (i) SEQUENCE CHARACTERISTICS:  
222 (A) LENGTH: 24 amino acids  
223 (B) TYPE: amino acid  
224 (D) TOPOLOGY: linear  
225  
226 (ii) MOLECULE TYPE: protein  
227  
228 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
229  
230 Met Ala Leu Ala Asp Leu Tyr Glu Glu Gly Gly Gly Gly Gly Glu 730  
231 1 5 10 15  
232  
233 Gly Glu Asp Asn Ala Asp Ser Lys  
234 20  
235  
236 (2) INFORMATION FOR SEQ ID NO: 9:  
237  
238 (i) SEQUENCE CHARACTERISTICS:  
239 (A) LENGTH: 474 base pairs  
240 (B) TYPE: nucleic acid  
241 (C) STRANDEDNESS: single  
242 (D) TOPOLOGY: linear  
243  
244 (ii) MOLECULE TYPE: DNA  
245  
246 (iii) HYPOTHETICAL: NO  
247  
248 (ix) FEATURE:  
249 (D) OTHER INFORMATION: Common IL-1ra sequence; a nucleotide G  
250 was added in the first position, for computer program  
251 reason, in order to encode the first amino acid Glu  
252 and further in order to avoid the creation of a stop  
253 codon in the inner region of the sequence  
254  
255 (ix) FEATURE:  
256 (A) NAME/KEY: CDS  
257 (B) LOCATION: 1..468  
258

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
PATENT APPLICATION **US/08/910,733**

DATE: 02/17/98  
TIME: 09:55:16

***INPUT SET: S23457.raw***

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Original Text